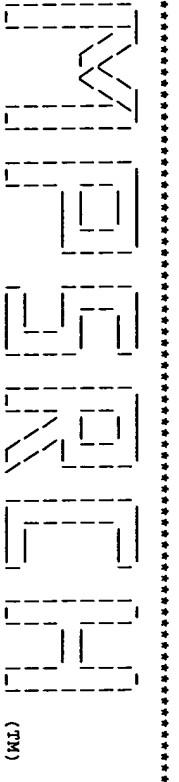


\*\*\*\*\*  
  
 \*\*\*\*\*

Release 3.1A John F. Collins, Biocomputing Research Unit.  
 Copyright (c) 1993-1998 University of Edinburgh, U.K.  
 Distribution rights by Oxford Molecular Ltd.

Run on: Wed Sep 2 19:06:54 1998; MasPar time 46.98 Seconds  
 660.285 Million cell updates/sec  
 lar output not generated.

Title: >US-09-052-855A-7  
 Description: (1-228) from US09052855A.seq  
 Perf. Score: 228  
 N.A. Sequence: 1 GTGAAAGAACATGTGGCGCAG.....TCTCTGACTGGGAGCTTC 228  
 Comp: CACHTTTTGTTACACCGGC.....AGAGACTGAGACCCCTCAGG

Scoring table: TABLE default  
 Gap 6  
 Nmatch 0% : Dbase 0; Query 0  
 Searched: 188442 seqs, 68026449 bases x 2  
 Post-processing: Minimum Match 0% summaries  
 Database:  
 n-genesee32  
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
 14:part14 15:part15 16:part16 17:part17 18:part18  
 19:part19 20:part20 21:part21 22:part22 23:part23  
 24:part24 25:part25 26:part26 27:part27 28:part28  
 29:part29 30:part30 31:part31 32:part32 33:part33  
 34:part34 35:part35 36:part36 37:part37 38:part38  
 39:part39 40:part40

istics:  
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	228	100.0	548	40	V16671	
2	226	99.1	548	27	T45883	
3	43	18.9	204	1	N81164	
4	41	18.0	91	9	Q51746	
5	41	18.0	204	1	N81164	
6	37	16.2	91	9	Q51746	
7	32	14.0	114	12	Q70469	
8	31	13.6	114	12	Q70469	
9	30	13.2	114	12	Q70469	
10	30	13.2	114	12	Q70469	
11	29	12.7	114	12	Q70465	
12	28	12.3	114	12	Q70466	
13	28	12.3	114	12	Q70466	

## ALIGNMENTS

RESULT 1  
 ID V16671; standard; cDNA: 548 BP.  
 AC V16671;  
 DR 22-JUN-1998 (first entry)  
 DE Polynucleotide sequence of a colon specific gene.  
 KW Colon-specific gene; probe; detection; expression; human;  
 KW diagnostic assay; colon cancer; antibody; screening; ss.  
 OS Homo sapiens.  
 FH Location/Qualifiers  
 KEY CDS  
 FT CDS  
 FT /\*tag= a  
 PN US5733748-A.  
 PD 31-MAR-1998.  
 PR 06-JUN-1995; US-469667.  
 PR (HUMA) HUMAN GENOME SCI INC.  
 PI Rosen, C.; Yu, G.;  
 DR WPI: 98-229823720.  
 DR P-PSDB: W46878.  
 PT Colon specific nucleic acids - useful as probes for detecting colon  
 PT cancer micrometastases  
 PS Claim 15; Fig 4; 51PP; English.  
 CC V16668-81 represent polynucleotide sequences of partial or full-length  
 CC cDNA clones of colon-specific genes. The polynucleotides can be used  
 CC as probes to detect expression of the corresponding human genes, e.g. in  
 CC diagnostic assays for detecting micrometastases of colon cancer.  
 CC Recombinant cells containing the polynucleotides can be used to  
 CC produce the polypeptides, in order that antibodies can be raised and  
 CC used in further screening or diagnostics.  
 SQ Sequence 548 bp;  
 Query Match 100.0%; Score 228; DB 40; Length 548;  
 Best Local Similarity 100.0%; Pred. No. 8; 8.3e-14;  
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 10 gtgaaaaacaaatgtggcaggccatcaaactcgccctgtgtgaatggaaacacggagct 69  
 |||||||









Best Local Similarity 94.2%; Pred. No. 7.00e-7; Mismatches 8; Indels 1; Gaps 1;

Matches 162; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

RESULT 3 ID Q51746 standard; cDNA: 91 BP.

ID Q51746; AC 31-MAY-1994 (first entry)

DT DE Oligonucleotide probe MK14-A

KW Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;

OS Synthetic.

PN EP-517911-A.

Query Match 22.8%; Score 42; DB 9; Length 91; Best Local Similarity 2.0%; Pred. No. 6.57e-10; Mismatches 1; Indels 0; Gaps 0;

Matches 1; Conservative 45; Mismatches 4; Indels 0; Gaps 0;

DB 12 svhsyvvhvshhsvhvvhvvhvsvvvvhvvhvvhvvhvvhvsvvc 61

CC ::::::::::::::::::::: ::::::::::::::::::::: ::::::::::::: ::::

CP 131 GCCCTGCCGGCTCTGACTCTTAAGCAGGCAGGAGCTTCAGCCCC 82

Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;

Query Match 22.8%; Score 38; DB 1; Length 204; Best Local Similarity 9.4%; Pred. No. 7.17e-08; Mismatches 10; Indels 55; Gaps 0; Gaps 0;

Matches 10; Conservative 55; Mismatches 41; Indels 0; Gaps 0;

DB 80 hvggcgyrttthhyrrmbrvdyrnsdaawvccyrrsvkydccbnnchhdhyvbb 139

QY 27 AGGGTGCATGCCCGAAGCCATTAGGGCTGACTCTAGGTAGTCAGAGC 86

DB 140 bbyvnnvhnnhnccecbnnhvhvnbnnhrnwvrvndarrdwv 185

PD 01-DEC-1993.

PR 24-MAY-1993; 108325.

PR 26-MAY-1993; US-889651.

PA (BECT ) BECKON DICKINSON CO.

PI Shank DD; Spears PA;

NP1; 93-37844/8.

PT New oligonucleotide probes specific for Mycobacteria nucleic acid in PT detection and amplification of Mycobacteria nucleic acid in samples

PS Claim 3; Page 14; 23bp; English.

CC Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14 (051735). It hybridized to all spp. of mycobacteria tested, but CC cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection.

CC See also Q51735,45 and Q51747,59.

CC Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;

RESULT 4 ID N831164 standard; DNA: 204 BP.

ID N831164; AC 08-NOV-1990 (first entry)

DT DE Base substituted E.coli beta-galactosidase alpha-fragment.

KW E.coli beta galactosidase alpha:fragment; base substitutions; ss.

OS Escherichia coli.

PR 03-APR-1987; US-034819.

PA (SUSO) SUOMEN SOKERI OY.

PI Lehtovaara P; Knowles J; Koivula A; Bamford J; Reinikainen T;

DR WPI; 88-279927/40.

PT Introducing random point mutations into nucleic acids -

PT by prep of single stranded template, annealing a primer, elongation, PT misincorporation, completion of molecules and screening.

PT Disclosure; P; English.

PS Random point mutations were introduced into the alpha fragment of CC E.coli beta-galactosidase. The wild type sequence was obtained as a CC single stranded template and an oligonucleotide was hybridised to CC it to generate a popn of DNA molecules which terminate at all CC possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system.

CC The sequence covers all 176 diff base substitutions, most of which CC occurred singularly in any given mutant.

CC See also P80375.

Sequence 204 BP; 21 A; 47 C; 17 G; 11 T; 108 Others;

Query Match 20.7%; Score 38; DB 1; Length 204; Best Local Similarity 9.4%; Pred. No. 7.17e-08; Mismatches 10; Indels 55; Gaps 0; Gaps 0;

Matches 10; Conservative 55; Mismatches 41; Indels 0; Gaps 0;

DB 80 hvggcgyrttthhyrrmbrvdyrnsdaawvccyrrsvkydccbnnchhdhyvbb 139

QY 27 AGGGTGCATGCCCGAAGCCATTAGGGCTGACTCTAGGTAGTCAGAGC 86